

**FIGURE 168**

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTGCAACCCTCTGGGCGTCCTTGTGGCCAATGTGCT  
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATAACCATCC  
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTCG  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA  
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGA CTGGACAGTGTCTCTGCTGCTGATGGCCGG  
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCCAGCACGGCGACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCCAGAGGGCCCCGGGAGCCCCCACCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

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**FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRTANMLATMSNPLGVLVANVLSPVLV  
KKGEDIPMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCLFSLACVPFALVSQLOQTALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMI FVLGQAE GILIMLMTALT VRRSEPSLSTCQQGEDPLDWT VSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

**Important features:****Potential Transmembrane domains:**

amino acids 30-50, 61-79, 98-112, 126-146, 169-182, 201-215, 248-268, 280-300, 318-337, 341-357, 375-387, 420-441

**N-glycosylation site.**

amino acids 40-43 and 43-46

**Glycosaminoglycan attachment site.**

amino acids 468-471

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**FIGURE 170A**

GTCCACATCCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCCATCATTTGCT  
GAAGTGGACCAACTAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTGG  
ACATCTCAGATCGCTTCCAATGAAGATGGCCTTGCCCTTGGGGTCTGCTTGTTCATAATCA  
TCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGGAAGGAGCACGGGGCTGATCAAGC  
CATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTTTCTGAATCTA  
GCCCCTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGG  
TGGCTACTTATTTCTTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAAATACCAAG  
TGTGAGAGGAAGTGCCATCTGGTACAGTGATCGGGAAGCTGTCCCAGGAACTGGGCGGGAG  
GAGAGGCGGAGGCAAGCTGGGGCCGCCTTCCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCAT  
TCAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCGGCTGGATCGAGAGCAGCTGT  
GCCGACAGTGGGATCCCTGCCTGGTTTCCCTTTGATGTGCTTGCCACAGGGGATTTGGCTCTG  
ATCCATGTGGAGATCCAAGTGCTGGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGA  
GCAGGAGCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACC CGATCCCCCTGGACAGAGCTC  
TTGACCCAGACACAGGCCCTAACACCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTT  
GCCTTGGATGTCATTGTGGGCCCTGATGAGACCAAACATGCAGAACTCATAGTGGTGAAGGA  
GCTGGACAGGGAAATCCATTCAATTTTTTGATCTGGTGTTAACTGCCTATGACAATGGGAACC  
CCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAGCCCT  
GCGTTTGCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCT  
CATAAAACTGACCGCCACAGACCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCCTCA  
GTAAGCACATGCCTCCAGAGGTGCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGTCTC  
ATTCTGCGTCGACCTCTAGACTATGAAAAGAACCCTGCCTACGAGGTGGATGTTTCAGGCAAG  
GGACCTGGGTCCCAATCCTATCCCAGCCCATTTGCAAAGTTCTCATCAAGGTTCTGGATGTCA  
ATGACAACATCCCAAGCATCCACGTACATGGGCCTCCCAGCCATCACTGGTGTGAGAAGCT  
CTTCCCAAGGACAGTTTTATTTGCTCTTGTGTCATGGCAGATGACTTGGATTGAGGACACAATGG  
TTTGGTCCACTGCTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCA  
ACACATACATGTTGCTAACCAATGCCACACTGGACAGAGAGCAGTGGCCCCAAATATACCCTC  
ACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATCAGCCAAGAAACAGCTCAGCATTC  
GATCAGTGACATCAACGACAATGCACCTGTGTTGAGAAAAGCAGGTATGAAGTCTCCACGC  
GGGAAAACAACTTACCCTCTCTTCACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGC  
ATTAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGA  
CTCCAACACAGGAGAGGTCACTGCTCAGAGGTCACTGAACTATGAAGAGATGGCCGGCTTTG  
AGTTCCAGGTGATCGCAGAGGACAGCGGGCAACCCATGCTTGCATCCAGTGTCTCTGTGTGG  
GTCAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGTCCAGCCTGTGCTCAGCGATGG  
AAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCCCATCGAGA  
CTCCCAATGGCTTGGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGG  
CCATTCCTTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCT  
CTACAGCATCCGCAATGGAAATGAAGCCACCTCTTCATCCTCAACCCTCATACGGGGCAGC  
TGTTTCGTCAATGTCACCAATGCCAGCAGCCTCATTGGGAGTGAGTGGGAGCTGGAGATAGTA  
GTAGAGGACCAGGGAAGCCCCCCTTACAGACCCGAGCCCTGTTGAGGGTCACTGTTTGTCAC  
CAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGATGCTGA  
CGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCCTGGCTTTGTTTCATGTCC  
ATCTGCCGGACAGAAAAGAAGGACAACAGGGGCTACAACCTGTCGGGAGGCCGAGTCCACCTA  
CCGCCAGCAGCCCAAGAGGCCCCAGAAACACATTCAGAAGGCAGACATCCACCTCGTGCCTG  
TGCTCAGGGGTCAGGCAGGTGAGCCTTGTGAAGTCGGGCAGTCCCACAAAGATGTGGACAAG  
GAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTTCCACCTCACCCGAC  
CCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGTGC  
TGCAAGACACGGTCAACCTCCTTTTCAACCATCCCAGGCAGAGGAATGCCTCCCGGGAGAAC  
CTGAACCTTCCCGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCTCTGAAGGTTGC  
AGGCAGCCCCACAGGGAGGCTGGCTGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCAC  
CAGCCTCCTCTGCAACCCTGAGACGGCAGCGACATCTCAATGGCAAAGTGTCCCTTGAGAAA  
GAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGCTGCCTTCGCCGA  
GCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTAGCAAATCTCCAGCTGC  
TGTCTTGCTGCATCAGGGCCAATTCCAGCCCCAACCAACCACCGAGGAAATAAGTACTTG  
GCCAAGCCAGGAGGCAGCAGGAGTGCAATCCCAGACACAGATGGCCCAAGTGCAAGGGCTGG

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**FIGURE 170B**

AGGCCAGACAGACCCAGAACAGGAGGAAGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGA  
AGCAACTGCTAGAGAAGAGCTGTCAAGTCTGCTGGACCCCAGCACAGGTCTGGCCCTGGAC  
CGGCTGAGCGCCCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCTCACCACCAACTA  
CCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGT  
TCGGCAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTC  
TCGGAGATGAGCTCACTGCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCCTGGAGGC  
CGCCTCCGAGGCGCTGCGGCGGCTCTCGGTCTGCGGGAGGACCCTCAGTTTAGACTTGGCCA  
CCAGTGACAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGGAAAGACGGGGACTGAGGGC  
AAGAGCAGAGGCAGCAGCAGCAGCAGCAGGTGCCTGTGAACATACCTCAGACGCCTCTGGAT  
CCAAGAACCAGGGGCCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACCTCAC  
TAGCTAGCGGCGGCCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAG  
CCCCAGGACTAACAGCTGACTGACCAAAGCAGCCCCTTGTAAGCAGCTCTGAGTCTTTTGGG  
GGACAGGGACGGTTTGTGGCTGAGATAAGTGTTTCCTGGCAAAACATATGTGGAGCACAAAG  
GGTCAGTCCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGGAAAGGGTGGCCTTCTT  
GGGTAGCAGGAGTCAGGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTATCAA  
TAAAGGAAAAGCAGTAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 171**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFVLDLATGDLALIHVEIQ  
VLDINDHQPFRFPKGEQELEISESASLRTRIPLDRALDPDTGPNLTHTYTLSPSEHFALDVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESS  
LALEIQEDAAPGTLTIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQQD  
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHADLGINGKVS  
YRIQDSPVAHLVAIDSNTEVTAQRSLNYEEMAGFEFQVIAEDSGQPMLASSVSVWVSLDDA  
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTT  
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREAESTYRQQPKRPQKHIOKADIHLVPVLRGQAGEPCEVGQSHKDVVDKEAMMEA  
GWDPCQLQAPFHLTPTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEPGGS  
RSAIPD TDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAAGMKVQGDPPGGKTGTGEGKSRGSS  
SSSRCL

**Important features:**

**Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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**FIGURE 172**

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGAATCTC  
ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATAACACTTACATGTCTTACTTCT  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG  
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT  
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT  
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA  
TACCGCACCATTAATCACTGAAGTCCTTGGGAACTGCAGTTCAACTTCTATCACCGTTGGTT  
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA  
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTTAAGGTTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAACAAAAAAGGGCGGCCGCGACTCTAGAGTTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

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**FIGURE 173**

MSFLIDSSIMITSQILFFGFGWLFEMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF  
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS  
SKSSNVIVLLLAQIMGMFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

**Important features:****Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

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**FIGURE 174**

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCCNGANACTATTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

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**FIGURE 175**

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC  
TTTNTTGAATTCCGGGTNNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN  
TAGGAGATCCCTTTCCCATTCTC

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**FIGURE 176A**

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGA  
TTTGCTACCTTTTTTGGCTCCCTGCTCGTCAACTGCTCTTCTCACGGGCTGTGCCTTCAAT  
CTGGACGTGATGGGTGCCTTGC GCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGT  
GGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGG  
CCCTGGCTCTTCTTGGG CAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGC  
CTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAGGAAAG  
CAAGGAGAACCAGTGGTTGGGAGTCAGTGTTCTGGAGCCAGGGGCCTGGGGGCAAGATTGTTA  
CCTGTGCACACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATG  
ATTGGTCGCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGA  
ATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTTGGGTTCTGCCAGCAGGGCA  
CAGCTGCCGCCTTCTCCCCGTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAAT  
TGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGA  
CGACGGTCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCCTCATCCCGGTCCCTG  
CCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTG  
AGCTTTGTGGCTGGAGCCCCCGCGCCAACCACAAGGGTCTGTGTGGTCATCCTGCGCAAGGA  
CAGCGCCAGTCGCCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTG  
GCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGGTGCC  
CCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGG  
GGGTCACTGGGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCCTGACTCCATGTTTCGGGA  
TCAGCCTGGCTGTCCTGGGGGACCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCC  
CCCTTTGATGGTGATGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGGGGTGTGCGCAA  
ACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTCAG  
GCAGCTTGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACACC  
GCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACG  
AAGCATCGACCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGG  
TCTGTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTG  
TTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCCGTGTGACGTTCCCTGAGCCG  
TAACCTGGAAGAACCCAAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCACCAGCATGACC  
GAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATT  
GTAGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGG  
GCTGCCTCCAGTGGCCCCCATCCTCAATGCCCACCAGCCCAGCACCCAGCGGGCAGAGATCC  
ACTTCCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAATCTGCAGCTGGTCCAC  
GCCCCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACCTCTGCCCATGGATGTGGATGG  
AACAACAGCCCTGTTTGCAGTGTGGG CAGCCAGTCATTGGCCTGGAGCTGATGGTCAACA  
ACCTGCCATCGGACCCAGCCAGCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTC  
CTGGTCATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAA  
GCCACTCTGCCTGTCCAATGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGA  
AGAGAGGTGCCCAGGTACCTTCTACCTCATCCTTAGCACCTCCGGGATCAGCATTGAGACC  
ACGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTC  
TGCACGAGCCCGTGTCTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCCCCAGC  
AACTCTTCTTCTCTGGTGTGGT GAGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGC  
AGCAAGGTCAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTCGCTCAGAACCCTGGGCTC  
TGCCTTCTCAACATCATGTGGCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAA  
TGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCTGGGCAGAAAGGGCTTTGCTCTCCAGGCCC  
AACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGCGGGAGCTGGAGCCACCTGA  
GCAGCAGGAGCCTGGTGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGCTG  
AGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAACCTGTGTGGTGTTCAGC  
TGCCCACTCTACAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAG  
CACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGGCCAACATCA  
CAGTGAAGTCCCTCCATAAAGAACTTGATGCTCCGAGATGCCTCCACAGTGATCCAGTGATG  
GTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGTGATCCTCCTGGC  
TGTA CTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCT  
TCAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGG  
GAAGACCGACAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAG

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**FIGURE 176B**

CCCCGGCGGGAGGGCCCGGATGCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGG  
GCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTCCCATGTCCCAGCCTGGCCTGTGG  
CTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTG  
GTGTCGCATCAAGATTTGGCAGGATCGGCTTCCTCAGGGGCACAGACCTCTCCCACCCACAA  
GAACTCCTCCCACCCAACCTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGAC  
AGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCCTGATGCAAAGGTGGGGAGAAGGGAT  
CCTAATCCCTTCCTCTCCCATTCACCCTGTGTAACAGGACCCCAAGGACCTGCCTCCCCGGA  
AGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCT  
AGTTTCCCCTCTCATCTGACCTTAGTTTGCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGTC  
TATTTATTAAAAAATATTTGAGAACAAAAAAAAAAAAAAAAAAAAA

**FIGURE 177**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL  
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFCG  
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEEELGGAVYVYLNQGGHWAGI  
SPLRLCGSPDSMFGISLAVLGD LNQDGFDPDIAVGAPFDGDGKVFYIYHGSSLGVVAKPSQVLE  
GEAVGIKSFGYSLSGSLDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSLSLQTPRLRRQAPGQGLPPVAP  
ILNAHQ PSTORAEIHFLKQCGCEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSDPAQPOADGDDAHEAQLLVMLPDSLHYS GVRALDPAEKPLCLSN  
ENASHVECELGNPMKRG AQVTFYLILSTSGIS IETTELEVELL LATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKEYVTVSNQGQSLRTLGS AFLNIM  
WPHEIANGKWL LYPMQVELEGGQGPQKGLCSRPNIHLHDVDSRDRRRRELEPPEQQEPGE  
RQEPSMSWVPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDR AAVLHVWGR LWNSTFLEEY  
SAVKSLEVIVRANITVKSSIKNLMLRDASTVIPVMVYLDPM AVVAEGVPWWVILLAVLAGLL  
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGS PRREGP  
DAHPILAADGHPELGPDGHPGPGTA

**Important features:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 1039-1064

**N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

**Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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**FIGURE 178**

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGGCGCGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAAACAAGATGCTCAAGGTGTCAGCCGTA CTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA  
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTGCGACGGCGGTAATTTTC  
TGGATGATAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTTCGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAACAGACTTGATACAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCCTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC  
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGTATAATTATTTGAAAATTCAGCTAAAGTTATAGAACTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTACGAGAACAACTTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTTGAAAG  
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAA

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**FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLLRPERSRFDTSILPI  
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPECQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSVGQCWCVDTRYGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

**Important features:****Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

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**FIGURE 180A**

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAA  
CAGTACCTGACGCCTCTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGC  
TGCCCTTCCCCGTGCTCCTTCTGGCCGCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGCCGGC  
TTCACACCTTCCCTCGATAGCGACTTCACCTTTACCTTCCCGCCGGCCAGAAGGAGTGCTT  
CTACCAGCCCATGCCCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTAGATGGAGCAG  
GATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAACCTTAGTTTTTGAACAAAGA  
AAATCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAA  
TACATTCAGCACCATTCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAG  
AACAGGCACAAGAACAAGAAGATTGGAAGAAATATATTACTGGCACAGATATATTGGATATG  
AAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCCAGACTAAGCAAAAGTGGGCA  
CATACAAATTCTGCTTAGAGCATTGGAAGCTCGTGATCGAAACATACAAGAAAGCAACTTTG  
ATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTTCATGGTGGTGGTGTCAGCCATTCAA  
GTTTATATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAACT  
AGAGTACGTAACATTGAAAAATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCAT  
TAATGGTCTTCTCCAAAATATTTTGAGATATAAAAGTAGGAAACAGGTATAATTTTAATGTG  
AAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAGTTGTACTTAAGTGTGTA  
ACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCATTTTC  
CTAACTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAAT  
TGCAACACCAGTCTGTTTTTAACAGGTTCTATTACCCAGAACTTTTTTGTAATGCGGCAGT  
TACAAATTAAGTGTGGAAGTTTTTCAGTTTTTAAGTTATAAATCACCTGAGAATTACCTAATGA  
TGGATTGAATAAATCTTTAGACTACAAAAGCCCACTTTTCTCTATTTACATATGCATCTCT  
CCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTGAGATTTTTATAACC  
AAATACATTTTCAGTGTAAATATTTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTCC  
CAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACAT  
GTTTTCTCTTTGAAATGAAGAATATAGTTTTAAAGCTTCCTCCTCCATAGGGACACATTTTC  
TCTAACCTTAACTAAAGTGTAGGATTTTAAATTAATGTGAGGTAAAATAAGTTTTATTTT  
TAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAATAATCATGTTATGTTAATTTTAAC  
ATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATATTGCTAAAATG  
ATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGG  
AAAGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAATTCACTTAAGTAGAACTAT  
AAATAAATATCTAGAATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGG  
AGATGATTAATTTCCAGTTAGCTGGAAGAACTTTGGCTGTAGGTTTTTATTTTCTACAAGA  
ATTCTGGTTTGAATTATTTTTGTAAAGCAGGTACATTTTATAAAATGTAAGCCCTACTGTAAG  
GTTTAGCACTGGGTGTACATATTTATTAAAAATTTTTATTATAACAACTTTTATTAAAAATGG  
CCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTT  
TTAAACACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGA  
AGTCTATGGGGGTCTTACTCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAATTT  
TTAAGTTATGCCCATTTATAACGTTGTTTATGACTACATTGTGAGTTAGAAACAACTTAA  
ATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATTCTTGATGAGCAATAATGA  
TAACCAGAGAGTGATTTCAATTTACACTCATAGTAGTATAAAAAGAGATACATTTCCCTCTTA  
GGCCCTTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAA  
TGCCGTATATGATCAATTACCTTAATTGGCCAAGAAATGCTTCAGGTGCTTAGGGGTATCC  
TCTGCAACACTTGCAAGAACAAGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTG  
CGCTGTTAAATTTGCAATGAGAAGCAAATTTACAGTACCATAACTAATAAAGCAGGGTACAG  
ATATAAACTACTGCATCTTTCTATAAAACTGTGATTAAGAATTCTACCTCTCCTGTATGGC  
TGTTACTGTACTGTACTCTGTACTCCTTACCTAACAATGAATTTGTTACATAATCTTCTAC  
ATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACTTCTTACCATATAAAAAC  
GATAATTGCTTTATTTGGAAAAGAAATTTAGGAATACTAAGGACAATTATTTTTTATAGACAAA  
GTAAAAAGACAGATATTTAAGAGGCATAACCAAAAAAGCAAACTTGTAACAGAGTAAAAA  
TCTTTAATATTTCTAAAGACATACTGTTTATCTGCTTCATATGCTTTTTTTTAAATTTCACTAT  
TCCATTTCTAAATTAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTTAACAGCTCATTT  
TGTCTTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTT  
CCATAATGTAGCAGTTACCGTGTTACCTCACACTAAGGCCTAGAGTTTGTCTGTATATGCA  
TTTGGATGATTAATGTTATGCTGTTCTTTTCATGTGAATGTCAAGACATGGAGGGTGTGTTGTA

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**FIGURE 180B**

ATTTTATGGTAAAATTAATCCTTCTTACACATAATGGTGTCTTAAAATTGACAAAAATGAG  
CACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTATGTGAAATTTTAAAAGACATTGA  
TTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTGCTCAAACG  
CTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATA  
ATAAAAATTATCAAAGGAAAA

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**FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFITLPAGQKECFYQPMPLKASLEIEY  
QVLGDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFTEL  
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN  
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

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**FIGURE 182**

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT  
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCCTGGATG  
CTGCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCC  
TTCTTTTTCCTTTTCTTCACCTTCATTTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 183**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS  
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

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**FIGURE 184**

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCAATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC  
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 185**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP  
FQGDSTVTKSCASKCKPSDVDGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

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**FIGURE 186**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA  
GACACTAAACCAGCTATCCAAATGCAGTGAACCTTTTATATAATAGATGCTATGAAAACC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAAGCATAACCCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

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**FIGURE 187**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGOVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSRLHTCQRH

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

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**FIGURE 188**

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

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**FIGURE 189A**

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATC  
CCGTGCGCCGCGGCTGGGCCGTCGGAGAGTGCCTTCTCTCTGACGCGGTGCTTGG  
GCTCGGCCAGGCGGGGTCCGCCGCCAGGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGAC  
CCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGAAGTATTAGAAATGAGCTGAAGAC  
CATTCACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCTTGAAGTAATG  
TAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTT  
CACTTAAATCAGAACTTGCATAAGAAAGAGAAATGGGAGTCTGGTTAAATAAAGATGACTATA  
TCAGAGACTTGAAAAGGATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGC  
ACAGATCAGGATTTTTACAGTTTACTTGGAGTGTCCAAACTGCAAGCAGTAGAGAAATAAG  
ACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAAAAACCCGAATAACCCAAATG  
CACATGGCGATTTTTTAAAAATAATAGAGCATATGAAGTACTCAAAGATGAAGATCTACGG  
AAAAAGTATGACAAATATGGAGAAAAGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAG  
CTGGAACATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGG  
AAAGAAGAGAATTTGATGCTGCTGTTAATTCTGGAGAAGTGTGGTTTGTAATTTTTACTCC  
CCAGGCTGTTACACTGCCATGATTTAGCTCCACATGGAGAGACTTTGCTAAAGAAGTGGA  
TGGGTACTTTCGAATTGGAGCTGTTAAGCTGTGGTGATGATAGAATGCTTTGCCGAATGAAAG  
GAGTCAACAGCTATCCAGTCTCTTCATTTTTTCGGTCTGGAATGGCCCCAGTGAAATATCAT  
GGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTCGCAATGCAGCATGTTAGAAGTACAGTGAC  
AGAACTTTGGACAGGAAATTTTGTCAACTCCATACAAACTGCTTTTGTCTGCTGGTATTGGCT  
GGCTGATCACTTTTTTGTTCAAAAGGAGGAGATTGTTTGACTTCACAGACGACTCAGGCTT  
AGTGGCATGTTGTTTTCTCAACTCATTGGATGCTAAAGAAATATATTTGGAAGTAATACATAA  
TCTTCCAGATTTTGAACACTTTTCGGCAAACACACTAGAGGATCGTTTGCTCATCATCGGT  
GGCTGTTATTTTTTTCATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAACTA  
AAAACCTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGACTGTTCTCTGCACCGA  
CATCTGTAGTAATCTGTATGTTTTTCAGCCGCTCTCTAGCAGTATTTAAAGGACAAGGAACCA  
AAGAATATGAAATTCATCATGGAAAGAAGATTCTATATGATATACTTGCCCTTTGCCAAAGAA  
AGTGTGAATTCTCATGTTACCACGCTTGGACCTCAAATTTTCTGCCAATGACAAAGAACC  
ATGGCTTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTACTACCAGAGTTAC  
GAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTCAT  
GAGGGACTCTGTAACATGTATAACATTCAAGGCTTATCCAACAACAGTGGTATTCAACCAGTC  
CAACATTCATGAGTATGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATC  
TTATGAATCCTTCAGTGGTCTCCCTTACACCCACCACCTTCAACGAAGTATTACACAAAGA  
AAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTGGTGTGTCATCCTTGCCAAGTCTT  
AATGCCAGAATGGAAAAGAATGGCCCGGACATTAAGTGGACTGATCAACGTGGGCAGTATAG  
ATTGCCAACAGTATCATTCTTTTTGTGCCAGGAAAACGTTCAAAGATACCCTGAGATAAGA  
TTTTTTCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGA  
TGCTTATTCCCTGAGAATCTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACAC  
CTCAGACTTTCAGTGAAAAGTCTTACAAGGGGAAAATCATTGGGTGATTGATTTCTATGCT  
CCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCTCTTGGCTAGGATGATTAA  
AGGAAAAGTGAAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAAAGCTG  
GGATCAGGGCCTATCCAAGTGTAAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAA  
GAAGAGCAGATAAATACCAGAGATGCAAAGCAATCGCTGCCTTAATAAGTGAAAATTTGGA  
AACTCTCCGAAATCAAGGCAAGAGGAATAAGGATGAACTTTGATAATGTTGAAGATGAAGAA  
AAAGTTTAAAAGAAATTTGACAGATGACATCAGAAGACACCTATTTAGAATGTTACATTTA  
TGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCAGAATTATCTACAGCA  
CTGGTGTAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTAGA  
CTTTGCAGGCTATAATATATGGTTCACACATGAGAACAAGAATAGAGTCATCATGTATTCTT  
TGTTATTTGCTTTTAAACAACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACA  
AAAGTAGGCTGGATTCAGTCCATGGACCATAGATTGCTGTCCCCCTCGACGGACTTATAATG  
TTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCTATCTACATAAATGTCTAAGTTGTAT  
AAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAGTTAGTTTTTGGTC  
ACTTGTTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTTAAACACCCA  
TGATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTT  
TTCTTTCTTCTCAAAGGTTGAAAAATGCTTTTTAATTTTTTACAGCCGAGAAACAGTGCAG

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**FIGURE 189B**

CAGTATATGTGCACACAGTAAGTACACAAATTTGAGCAACAGTAAGTGCACAAATTCTGTAG  
TTTGCTGTATCATCCAGGAAAACCTGAGGGAAAAAAATTATAGCAATTAAGTGGGCATTGTA  
GAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATATGTGTTTCA  
GTATTTTCTGAAATTGCTTTCATAGAAATTTTCCCACTGATAGTTGATTTTGTAGGCATCTA  
ATATTTACATATTTGCCTTCTGAACCTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTT  
TTCTTTCATAGTTTTTGGTTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAAT  
TACTTTACAGGTTGTTTTACTGTAGCTTATAATGATACTGTAGTTATTCAGTTACTAGTTT  
ACTGTCAGAGGGCTGCCTTTTTTCAGATAAATATTGACATAATAACTGAAGTTATTTTTATAA  
GAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGACTCAA  
GAATCACAAATTTGTCAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGT  
AAAAATCCAATCAGTCAAAAGAGGTCAATGAATTAAAAGGCTTGCAACTTTTTCAAAAAA  
AAAAA

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**FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYRYDFGI  
YDDDPEIITLERREFDAAVNSGELWVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS  
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN  
TLEDRLAHRWLLFFHFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP  
SLAVFKGQGTKEYEIHGKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS  
AEQILEFIEDLMNPSVVS LTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG  
FLPQVSTDLTPTQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPFEFELLARMIKGKVKAGKVDC  
QAYAQTQCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

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**FIGURE 191**

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA  
GTCGTTGGTGAAGTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT  
GGGAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCACCA  
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTCTGAG  
ACTACAGAAGTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTTGAATCAATGCTGCAAAGCTTTATTTTCACATTTTT  
TCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCTCTT  
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT  
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAGATTGAGCATTGAAAGATTTCCCTAGCCTCTTCTCTTT  
TCATTAGCCCAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAGTGGACCCTCTATATTTCTCCCTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT  
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA  
CAATGGACCCAAGAGAAGAA

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**FIGURE 192**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTFEFAKRQSI  
LVLWDINKRGVEETAAECKRLGVTAHAYVVDSCNREEIYRSLNQVKKEVGDTVIVVNNAGTV  
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFNVTGFTKNPSTRLWPVLETDEVVRSLID  
GILTNNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

**Important features:**

**Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

**Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

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**FIGURE 193**

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCGCCGGGGC  
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT  
GCTGATCATCGTGACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACAGTCCTTCT  
CTAGGCCGCACACGGGGCCGCGCTGCCACGCCCCGGGCCGACAGGGACAGGGAGCTCACG  
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA  
CGTGACACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC  
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC  
GAGACTGAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC  
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

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**FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGVSVMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELT  
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFTKERAFFDDIPNSELHIVDDRHGAIYCYVPKVACTNWKRMIVLS  
GSLHHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAQLLQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

**Important features:**

**Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

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**FIGURE 195**

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCTGGTTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG  
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCTTGGCCTCCGA  
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCAGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCCGATATCCCTTCTGATTTCTCTCATTT  
CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACCTCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT  
AAAAACGATTTGCAGCC

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**FIGURE 196**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPQORPEETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISLVLGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAVFLASEANFCTGIELLVTGG  
AELGYGCKASRSTPVDAPDIPS

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

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**FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTG  
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACC  
TGGTGTACAGGATGAAACCGTATGCCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCCCTGTGCGCCGCCG  
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA  
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

**FIGURE 198**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCL  
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

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**FIGURE 199**

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG  
GCGCCCAACATGGCGGGGTGGGCGCTGCGGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT  
CGCGGCTGTGGCGGCGACGGCAGGCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG  
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT  
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAAGAATGGGAGGCTTTTGCAAAGAA  
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG  
GCCGCTTCTTTGTCACCACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT  
TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACCTATTTACAGTGACTCTTGGAATT  
CCTGCTTGGTGTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTGGCCTTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA  
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG  
CTGGTGTGGATGAGGAGAGAAAGTGAGGCCAATGATCAGGGGGCCCCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC  
TGACACAGAGGTGGTGGAAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC  
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAAATCCTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAAGATGCT  
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT  
GACAAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCCTTTTCTTGTGTAAAGTATTTAT  
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTGAGGCTCT  
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTTT  
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT  
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGGTCCCTGGGTCTTGAAC  
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCCTTCAGTGATGTGCTTTTGGTGAAA  
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTGTTTCCATCTTCTGTAATC  
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTTCTTT

**FIGURE 200**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMASNWTLMEGEWMLKIFYAP  
WCPSCQQT DSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSEERSEQNRRSEEAHRAEQLODAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSHADKGL

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

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**FIGURE 202**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

**Important features:**

**Type II transmembrane domain:**

amino acids 45-65

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

**N-myristoylation sites.**

amino acids 35-40 and 151-156

**Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

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**FIGURE 203A**

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGG  
TCTCGCTCTGTACACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACC  
TCCCGGGTTCAAGTGATTCTCATGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGAC  
TTCCAAGAGTGACTCCGTCGGAGGAAAATGACTCCCCAGTCGCTGCTGCAGACGACACTGTT  
CCTGCTGAGTCTGCTCTTCCCTGGTCCAAGGTGCCACGGCAGGGGCCACAGGGAAGACTTTC  
GCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGAC  
CTGCGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCCTTTCCTGCGAGC  
CCACCCTGCTTCCCGATCCTTCCCTGACCCAGGGGCCTCTACCACTTCTGCCTCTACTGGA  
ACCGACATGCTGGGAGATTACATCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTGACAAA  
GCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTGGCTCAGGGCCCCCGCTGTT  
AGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCCGCCAGCT  
TCACCTTCTCCTTCCACAGTCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACATGTGC  
GAGCTCAAAAGGGACCTCCAGCTGCTCAGCCAGTTCTGAAGCATCCCCAGAAGGCCTCAAG  
GAGGCCCTCGGCTGCCCCCGCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTG  
TGAGATTCAATGGGGGACATGGTGTCTTTCGAGGAGGACCGGATCAACGCCACGGTGTGGAAG  
CTCCAGCCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGGCAGGAGGAGGAGCAGAG  
CGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGCCGGA  
GCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGAC  
AAGAATTCCAGCCAAGTCTTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGT  
AGCCAACCTCACGGAGCCCGTGGTGTCTACTTTCAGCACCAGCTACAGCCGAAGAATGTGA  
CTCTGCAATGTGTGTTCTGGGTGAAGACCCACATTGAGCAGCCCGGGGCATTGGAGCAGT  
GCTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGCAACCACTTGACCTA  
CTTTGCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGCC  
TCCTCTCCTACGTGGGCTGTGTCTCTGCCCCTGGCCTGCCTTGTACCATTGCCGCCTAC  
CTCTGCTCCAGGGTGCCCTGCGGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCA  
CATGAACCTGCTGCTGGCCGTCTTCTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGG  
CCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCCATCTTCTGCACTTCTCCCTGCTC  
ACCTGCCTTTCCTGGATGGGCCCTCGAGGGGTACAACCTCTACCGACTCGTGGTGGAGGTCTT  
TGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCT  
TTCTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACCTATGGCCCCATCATCTTGGCTGTG  
CATAGGACTCCAGAGGGCGTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAG  
CTACATCACCAACCTGGGCCTCTTACGCCTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCA  
CCATGGTGGTGCAGATCCTGCGGCTGCGCCCCACACCCAAAAGTGGTCACATGTGCTGACA  
CTGCTGGGCCTCAGCCTGGTCTTGGCCTGCCCTGGGCCTTGATCTTCTTCTCCTTTGCTTC  
TGGCACCTTCCAGCTTGTCTGCTCTACCTTTTCAGCATCATCACCTCCTTCCAAGGCTTCC  
TCATCTTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCCTCCCTCTGAAG  
AGCAACTCAGACAGCGCCAGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTA  
GGCCTCCAGCCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTCGTCGCACACTGCCTGT  
GGCCCCCGAGCCAGGCCAGCCCCAGGCCAGTCAGCCGCAGACTTTGGAAAGCCCAACGACC  
ATGGAGAGATGGGCCGTTGCCATGGTGGACGGACTCCCGGGCTGGGCTTTTGAATTGGCCTT  
GGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTA  
GGGTACTGTCCCCACATCTGTCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTG  
GGCCAGCCCTCATTGCTGGGGGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATC  
CTGTGCCCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTCACCCTGA  
GGGCACTCTGCATCCTCTGTCAATTTAACTCAGGTGGCACCCAGGGCGAATGGGGCCAGG  
GCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTGGCAGGAGCACAGCAGCAG  
CTCGCCTACCTCTGAGCCCAGGCCCCCTCCCTCCCTCAGCCCCCAGTCTCCTCCATCTT  
CCCTGGGGTTCTCCTCCTCTCCCAGGGCCTCCTTGCTCCTTCGTTACAGCTGGGGGTCCCC  
GATTCCAATGCTGTTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGT  
TTGTCTACTGCACAAGCCTCGGCCTGCCCTGAGCCAGGCTCGGTACCGATGCGTGGGCTGG  
GCTAGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTGCTCACCTGACC  
AAGCACACGCCTCAGAGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAAGTGTGG  
ACCATGCCAGTCCCGTCTGGTTTCCATCCCACTCCAAGGACTGAGACTGACCTCCTCTG  
GTGACACTGGCCTAGAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAATAGCTC

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**FIGURE 203B**

CAGGCGCCCTCGGCCGCCCATCATGGTTAATTCTGTCCAACAAACACACACGGGTTAGATTGC  
TGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACTCCTCCTGCCAACATTC  
AGTCTGGTATGTGAGGCGTGCGTGAAGCAAGAAGCTCCTGGAGCTACAGGGACAGGGAGCCAT  
CATTCCTGCCTGGGAATCCTGGAAGACTTCCTGCAGGAGTCAGCGTTCAATCTTGACCTTGA  
AGATGGGAAGGATGTTCTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAAAAGAAGTA  
CATGTTTATTGTAGAGAATTTGGAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAATCAG  
CTGTTGTAATCGCCTAGCAA  
AAA

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**FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFSQQRNQTHRSSLHYKPTPDLRISIENSE  
EALTVHAPFPAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTHSFHSPPHATAAHNASVDMCELKRDQLL  
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTLFRQTKGRSGEAEKRLLLVDVFSSQALFQDKNSSQVLGE  
KVLGIVVQNTKQVANLTPVVLTFQHQLQPKNVTLCVFWVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVVSALACLVTIAAYLCSRVPPLPC  
RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLE  
GYNLYRLVVEVFQTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY  
PSMCWIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLLFIWYWSMRLQARGGPSPLKSNSDSARLP  
ISSGSTSSSRI

**Important features:****Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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**FIGURE 205**

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTTCCTGTTCAACATGG

**FIGURE 206**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCA  
GGTTTTGCTTTGATCCTTTTCAAAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTT  
GGATGGGATTATGTGGAACTACCCTGCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCC  
ACCCAGTGACAGCCTTCCCCTGGCGGTGGTGAAAGAGACTCGGGAGTCGCTGCTTCCAAAGT  
GCCCCGCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGCT  
GACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAAT  
TCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATT  
ACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTTCTCATACTTATCCAAGAAATAC  
GGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACCTTACGTTTGATG  
AAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAG  
GAACCCAGTGATGGAACATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAGGAAAACA  
GATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAAC  
CAGGGTTCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCCTTCA  
GTGCTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTAC  
CTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTAT  
ATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTTTGGAGAAAATCCAGAGTGGTG  
GATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGT  
GTCCATAAGGGGAAGAACTAAAGAGAACCGATACCATTTTTCTGGCCAGGTTGTCTCCTGGTTA  
AACGCTGTGGTGGGAACCTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCA  
AGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGG  
ATTGCACAAATCACTACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCA  
GAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCACTGC  
AGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTT  
CAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATT  
AGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATC  
GTGGAAAGAAAATTAATGTTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTA  
CGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGT  
ACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCC  
ATGTCCTGGGCCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGCTCATATTCAC  
ATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATGTTGCT  
ATGAATTAACTTGTGTCTGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAAAT  
TTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAG  
AGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTAT  
ATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTAC  
CAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTCAGTTGGTAAATT  
TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGAC  
AAAAATACATGTATTTTCACTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAA  
CTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATC  
TTCCATTCTGTATTGAGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTGAGATCC  
AGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGC  
ACCTTGAAAAGAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACAT  
CCTATTATTGTGATGTTGTGGTTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAAT  
ACATGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCA  
ATTTAAAAGAAAATCAGTAAAATATTTTGCTTGTAATAATGCTTAATATNGTGCCTAGGTTAT  
GTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAGAATGTGGCTATTTTG  
GGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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**FIGURE 207**

MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPKGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL  
NNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLY  
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQ  
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG

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**FIGURE 208**

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATT  
CCATTTTGGGAAGAAGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTCTTA  
TCCTTTTAAACATAATCCTAATTTCCAAACTCCTTGGGGCTAGATGGTTTCTTAAACTCTG  
CCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTGATCGTGGACTGCACAGACAAGCA  
TTTGACAGAAATTCCTGGAGGTATTCCCACGAACACCACGAACCTCACCTCACCATTAACC  
ACATACCAGACATCTCCCCAGCGTCCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTT  
AGATGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCA  
GATTAAACCCAGAAGCTTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACC  
AGCTACTAGAGATACCGCAGGGCCTCCCGCCTAGCTTACAGCTTCTCAGCCTTGAGGCCAAC  
AACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCCAACATAGAAATACTCTACCT  
GGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAAGATGCCT  
TCCTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCT  
ACTGTTTTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCA  
AGAAGATGATTTTAATAACCTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTC  
GTTGTTATAATGCCCCATTTCTTGTGCGCGTGTAAAAATAATTCTCCCTACAGATCCCT  
GTAAATGCTTTTGATGCGCTGACAGAATTAAAAGTTTTACGTCTACACAGTAACTCTCTTCA  
GCATGTGCCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACTGGATCTGTCCCAA  
ACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAA  
TTGGATCTGTCTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGC  
ATTTTCTTCACTGAAAAGCCTGAAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGA  
AAAGCTTTAACCTCTCGCCATTACATAATCTTCAAAATCTTGAAGTTCTTGATCTTGGCACT  
AACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGACTGAAAGTCATAGA  
TCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAATG  
CCAGAACTTCTGTAGAAAGTTATGAACCCCAGGTCCTGGAACAATTACATTATTTTCAGATAT  
GATAAGTATGCAAGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGA  
AAGCTGCTACAAGTATGGGCAGACCTTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGT  
CCTCTGATTTTTCAGCATCTTTCTTTCCTCAAATGCCTGAATCTGTGAGGAAATCTCATTAGC  
CAAACCTCTTAATGGCAGTGAATTCCAACCTTTAGCAGAGCTGAGATATTTGGACTTCTCCAA  
CAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGG  
ATATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACC  
AAGAACCTAAAGGTTCTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAG  
CAGGACCATGGAGAGTGAGTCTCTTAGAACTCTGGAATTCAGAGGAAATCACTTAGATGTTT  
TATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAGAATCTGCTAAAATTAGAGGAA  
TTAGACATCTCTAAAATTCCCTAAGTTTCTTGCCCTTCTGGAGTTTTTGTATGGTATGCCCTCC  
AAATCTAAAGAATCTCTCTTTGGCCAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCC  
AGTGCTAAAGAACCTGGAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAG  
AGATTATCCAACCTGTTCCAGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAG  
TCTGACGAAGTATTTTCTACAAGATGCCTTCCAGTTGCGATATCTGGATCTCAGCTCAAATA  
AAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTCAACAATCTGAAGATGTTG  
CTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTTGTCTGGTGGGTAA  
CCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCAC  
ACAAGGGCCAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTG  
ATTCTGTTCTCACTTTCCATATCTGTATCTCTCTTCTCATGGTGATGATGACAGCAAGTCA  
CCTCTATTTCTGGGATGTGTGGTATATTTACCATTTCTGTAAGGCCAAGATAAAGGGGTATC  
AGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTATGACACTAAAGACCCA  
GCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAACA  
TTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTT  
CCCAGAGCATAAGCTTAGCAAAAAGACAGTGTTTGTGATGACAGACAAGTATGCAAAGACT  
GAAAATTTTAAGATAGCATTTTACTTGTCCCATCAGAGGCTCATGGATGAAAAGTTGATGT  
GATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAGTCCAAGTTCCCTCCAGCTCCGGAAAA  
GGCTCTGTGGGAGTTCTGTCTTGAGTGGCCAACAACCCGCAAGCTCACCCATACTTCTGG  
CAGTGTCTAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGA  
AACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

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**FIGURE 209**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRNCNCPVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYR  
NPCYVSYSIEKDAFLNLTKLKVLSLKDNVTA VPTVLPSTLTELYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPFRWF  
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO  
TDLDSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSL  
AKNGLKSFWSKKLQCLKNLETLDLSHNQLTTVPERLSNCSRLKNLILKNNQIRSLTKYFLO  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDVWVFWVWNHTEVTIP  
YLATDVTVCVGPAGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLLEE  
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIIILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

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**FIGURE 210A**

GGGTACCATTTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAA  
AACATGTTTCCTTCAGTCGTCAATGCTGACCTGCATTTTCCTGCTAATATCTGGTTCCTGTGA  
GTTATGCGCCGAAGAAAATTTTTCTAGAAGCTATCCTTGTGATGAGAAAAAGCAAATGACT  
CAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAGTTCCCCAAACGGTGGGCAAATAT  
GTGACAGAACTAGACCTGTCTGATAATTTTCATCACACACATAACGAATGAATCATTTCAAGG  
GCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAA  
ATCCCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCTCAACCTAAAAAAC  
CTAAGGGAGTTACTGCTTGAAGACAACCAGTTACCCCAAATACCCTCTGGTTTGCCAGAGTC  
TTTGACAGAACTTAGTCTAATTCAAACAATATATACAACATAACTAAAGAGGGGCATTTCAA  
GACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAAGTCTATTTTAAACAAAGTTTGCGAG  
AAAACATAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTATCACTATC  
TTTCAATTCTCTTTCACACGTGCCACCCAAACTGCCAAGCTCCCTACGCAAACCTTTTTCTGA  
GCAACACCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTA  
CTAGATTTAAGCGGGAAGTGTCCGAGGTGCTTCAATGCCCCATTTCCATGCGTGCTTGTGA  
TGGTGGTGCTTCAATTAATATAGATCGTTTTGCTTTTCAAACCTTGACCCAACTTCGATACC  
TAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGTTTAAAAATATGCCTCAT  
CTGAAGGTGCTGGATCTTGAATTCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCATTTTT  
AACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATC  
CACAGCATATTAATATTTCCAGAACTTCTCTAACTTTTGTCTCTACGGGCATTGCAATTA  
AGAGGTTATGTGTTCCAGGAAGTCAAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAAA  
CTTATCGACTATCAACTTGGGTATTAATTTTATTAAGCAAATCGATTTCAAACCTTTTCCAAA  
ATTTCTCCAATCTGGAAATTATTTACTTGTGAGAAACAGAAATATCACCGTTGGTAAAAGAT  
ACCCGGCAGAGTTATGCAAATAGTTCCTCTTTTCAACGTCATATCCGGAAACGACGCTCAAC  
AGATTTTGAGTTTGACCCACATTCGAACCTTTTATCATTTACCCGTCCTTTAATAAAGCCAC  
AATGTGCTGCTTATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCA  
AACCAATTTGAAAATCTTCTGACATTGCCTGTTTAAATCTGTCTGCAAATAGCAATGCTCA  
AGTGTTAAGTGGAAGTGAATTTTCAGCCATTCCTCATGTCAAATATTTGGATTTGACAAACA  
ATAGACTAGACTTTTGATAATGCTAGTGCTCTTACTGAATTGTCCGACTTGGAAGTTCTAGAT  
CTCAGCTATAATTCACACTATTTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATTCA  
AAATTTACAAATCTAAAAGTTTTAACTTGAGCCACAACAACATTTTATACTTTAACAGATA  
AGTATAACCTGGAAAGCAAGTCCCTGGTAGAATTAGTTTTTCAGTGGCAATCGCCTTGACATT  
TTGTGGAATGATGATGACAACAGGTATATCTCCATTTTCAAAGGTCTCAAGAATCTGACACG  
TCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATGAAGCATTCTTAAATTTGCCAG  
CGAGTCTCACTGAACTACATATAAATGATAATATGTTAAAGTTTTTTAACTGGACATTACTC  
CAGCAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTAACTGA  
TAGCCTATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCC  
ACCTACCTCTGGCTTTCTTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAAT  
CTGCTAAAAACAATCAACAAATCCGCACTTGAACTAAGACCACCACCAAATTATCTATGTT  
GGAAGTACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAGATTTCCGAAGATGGATGG  
ATGAACATCTGAATGTCAAATTTCCAGACTGGTAGATGTCATTTGTGCCAGTCTGGGGAT  
CAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACCTTGTGTTTCAGATGTCACTGCAGT  
GATATTATTTTCTTCACGTTCTTTATCACCAACATGGTTATGTTGGCTGCCCTGGCTCACC  
ATTTGTTTTACTGGGATGTTTGGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTAC  
AGGTCTCTTTCCACATCCCAAACCTTTCTATGATGCTTACATTTCTTATGACACCAAAGATGC  
CTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAGAGAGCCGAGACAAAA  
ACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACCTC  
ATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAG  
CTGGAACCTTTAAAACAGCTTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATG  
TGATTATATTTATCCTGCTGGAGCCAGTGTACAGCATTCTCAGTATTTGAGGCTACGGCAG  
CGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACAACCCGAAGGCAGAAGGCTTGTTTTG  
GCAAACCTCTGAGAAATGTGGTCTTGACTGAAAATGATTCACGGTATAACAATATGTATGTCG  
ATTCCATTAAGCAATACTAACTGACGTTAAGTCATGATTTTCGCGCCATAATAAAGATGCAAA  
GGAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATATCCCAAAACCTTAGTGG  
TTTAAACAACACATTTGCTGGCCACAGTTTTTGAGGGTCAGGAGTCCAGGCCCAGCATAA

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**FIGURE 210B**

CTGGGTCCTCTGCTCAGGGTGTCTCAGAGGCTGCAATGTAGGTGTTCAACCAGAGACATAGGC  
ATCACTGGGGTCACACTCATGTGGTTGTTTTCTGGATTCAATTCCTCCTGGGCTATTGGCCA  
AAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCCACAAGGCAGCTTGCTTCATCAGAGCT  
AGCAAAAAGAGAGGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAATCGAATCAAAAAG  
TGATATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCCACCAGCT  
CCATGGGAGTGACCACCTCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGAT  
TGCTTCAGTTGGTCATCAACTATTTCCCTTGACTGCTGTCCTGGGATGGCCTGCTATCTTG  
ATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACCATCTTAGCAGTTGACCTAA  
CACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCTAATATTAAGC  
TGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTCG  
GTTTTATTTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTAGATG  
CCATTTAAGAACTGAGATGGATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAA  
GTATGCAGCTAAATTCGAAGCTTTTGGTCTATATTGTTAATTGCCATTGCTGTAAATCTTAA  
AATGAATGAATAAAAATGTTTCATTTTACAAAAA

**FIGURE 211**

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPCDEKKQNDSVIAECSNRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFSLNTQIKYISEEDFKGLINL  
TLDDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTLQRYLNLSSSTSLRKINAAWFKNM  
PHLKVLDLEFNVLVGEIVSGAFLTMLPRLEILDLSFNLIKGSYPQHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFSLNLEIIYLSENRISPLV  
KDTRQSYANSSSFQRHIRKRRSTDFFEDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDELEV  
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDSLNLRLKHIPNEAFLNLPASLTE LHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDLS  
SNLLKTINKSALETKTTTKLSMLELHGPNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQTFFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIID  
NMQSINQSKKTVFVLTKKYAKSWNEKTA FYLALQRLMDENMDVII FILLPEVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGLEFWQTLRNVL TENDSRYNMYVDSIKQY

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**FIGURE 212**

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCCGTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCCTGGAGGCACAGGCCAATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGGTGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCCGGCCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA  
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGACAGTGCAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC  
CCCCTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCCTG  
GAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG  
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC  
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG  
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA  
AAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTTGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

**FIGURE 213**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

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**FIGURE 214**

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTTCAGCTTGGCTGGGCCCCGCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGGCCCCGGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCCG  
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG  
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACCTCCTCCAGCAGCTCGGCCGCATCGAC  
TCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGA  
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCCTCCTCTTCCTCCTCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA  
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC  
CCCCAGCACATAAAAATGAAACGTG

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**FIGURE 215**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSadgtLCVpKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

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**FIGURE 216**

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTTGGGAGGGGACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG  
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCCTCC  
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCCTTCCTGGAGGAGCAGCT  
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCTTCCTCGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTG

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**FIGURE 217**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSadgtLCVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

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**FIGURE 218**

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCTTGTCAGGAGGAGACAGCCTC  
CCGGCCCCGGGGAGGACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTC  
CGTTTCCTGCCGTGAGCTGCCGGCCGAGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTC  
CTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGGAGATTGTCTTCCAGGGCTAGCAA  
TTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGATTTCAAAGCTG  
GGCTCAGCCTCTGTTTCTTCTCTCGTGTAATCGCAAAACCCATTTTGGAGCAGGAATTCCAA  
TCATGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAACTCCCAGGCAGG  
AACACCTTTTGCTGTGATGGCCGCGTCATGATGGCCCGGCCAAAAGGGCATTCTTCTACCTGAC  
CCTTTTCCTCATCCTGGGGACATGTACACTCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTG  
TTCAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCTTCCTTTTCTCCATGGCTACA  
CTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCGGGCGCTACCAGATGAAGCAGC  
TTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGC  
CTCGTATCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGC  
AAGATCTTCCGGCCTCCCCGGGCCTCCCATTGCAGCATCTGTGACAACCTGTGTGGAGCGCTT  
CGACCATCACTGCCCCCTGGGTGGGGGAATTGTGTTGGAAAGAGGAACTACCGCTACTTCTACC  
TCTTCATCCTTTCTCTCTCCCTCCTCACAACTCTATGTCTTCGCCTTCAACATCGTCTATGTG  
GCCCTCAAATCTTTGAAAATTTGGCTTCTTTGGAGACATTGAAAGAAACTCCTGGAACCTGTTCT  
AGAAGTCCTCATTTGCTTCTTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCTACTT  
TCCTCGTGGCTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGGAAGAAT  
CGCGTCCAGAATCCCTACAGCCATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGG  
CCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTATTTTGCCACTGGAGGAAAGTGGAAGTC  
GACCTCCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCCCAGCCCCCACAGAA  
CACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAGA  
GCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACT  
TTTGTGTTGTGTTAATTAGGGCTATGAGAGATTTTCAGGTGAGAAGTTAAACCTGAGACAGAG  
AGCAAGTAAGCTGTCCCTTTTAACTGTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTG  
GCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACTCAAGGCAGTGGCAGAAAGATGTCAG  
TCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCTCCATGGCCTCA  
GCCACAGGGTCCCCTTGGACCCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTC  
ACTGGTCTCATTCTGGGGCTAAAAGTTTTTGGAGACTGGCTCAAATCCTCCCAAGCTGCTGCA  
CGTGCTGAGTCCAGAGGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTTGG  
GGTCTTCAGGACTGAAGAGGAGGGAGAGTGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCC  
AGCATTGCCACAAATCCTTTTAGGAATGGGACAGGTACCTTCCACTTGTTGTANNNNNNNN  
NNNNNNNNNNNNNNNNNNNTTGTTTTTCTTTTGAATCCTGCTCCCATTAGGAGCAGGAATG  
GCAGTAATAAAAGTCTGCACTTTGGTCAATTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACT  
TAAACACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGG  
AAACCAAGGCACAGAGAGGCTCTCCTCTCCTCTCCTCTCCCCGATGTACCTCAAAAAAAA  
AAAAATGCTAACCAGTTCTTCCATTAAGCCTCGGCTGAGTGAGGGAAAGCCCAGCACTGCTG  
CCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCTATGGTAACCACACTGGGG  
GCTTCTTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTTCACCC  
TGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTTCAAGGAAGAAG  
ATTTATGTATTATATGTGGCTATATTTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAG  
GGTCTGTCTGGATGACTTATGCGGTGGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAA  
GGCGATTAACTGTGTCTAATGCA

**FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAV.  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGN CVGKRNYRYFYL  
FILSLSLLLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLI CFFTLWSVVG LTGFHTF  
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMP PPEPPEPPQEAAEAEK

**FIGURE 220**

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCCTTTCT  
CCCACAGAGCNCCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT

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**FIGURE 221**

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

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**FIGURE 222**

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAV  
PSAEFQWYKDDKRLIEGKKG VKVENRPFLSKLI FFNVSEHDYGN YTCVASNKLGHTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLL LKF

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**FIGURE 223**

GAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

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**FIGURE 224**

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGCGGCCCGGGAGCGGGCCAGCTG  
CCGGGAGCCCTGAATCACCGCCTGGCCCGACTCCACCAATGAACGTCGCGCTGCAGGAGCTGG  
GAGCTGGCAGCAACGTGGGATTCCAGAAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAG  
CTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCTGCACTGCTTCTGGGCTGCCTTGT  
GGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACAGAGGCCTGCA  
TTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCCTGTGAGGACTTT  
TACCAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTG  
GAACACCTTCAACAGCCTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACA  
CCACCTTCAACTCCAGCAGTGAAGCTGAGCAGAAGACACAGCGCTTCTACCTATCTTGCCTA  
CAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGAGACCTCATTGAGAAGATTGG  
TGTTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAGGCAGTAG  
CAGGGACCTACAGGGCCACCCCATCTTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCC  
AACAGCAATGTTATCCAGGTGGACCACTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTT  
AAACAGAACTGCCAATGAGAAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACTGGGGA  
TGCTGCTGGGTGGGCGGGCCACCTCCACGAGGGAGCAGATGCAGCAGGTGCTGGAGTTGGAG  
ATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGGACGAGGAGAAGATCTACCA  
CAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTCTGT  
CTTTCTTGCTGTCACCATTTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGAT  
TATTTGCAGCAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCT  
GATCTGGAACCTGGTGCAAAGACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAG  
AGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAGTCCTGTGTGCCGAGGTGGCAGACCTGC  
ATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTCGTGAAGGCCACGTT  
TGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAGG  
AGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCA  
GATGCCATCTATGATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGA  
TGTTTATGACGGGTACGAAATTTCTGAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACA  
ACTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAGCCTCCCAGCCGAGACCAGTGGAGC  
ATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATCGTCTTCCCCGC  
TGGCATCCTGCAGGCCCCCTTCTATGCCCCGAACCACCCCAAGGCCCTGAACTTCGGTGGCA  
TCGGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGAC  
AAAGAAGGGAACCTGCGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACAC  
GGCCTGCATGGAGGAACAGTACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCC  
AGACGCTGGGGGAGAACATTACTGACAACGGGGGGGCTGAAGGCTGCCTACAATGCTTACAAA  
GCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTACCAACCACCA  
GCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACG  
AGGGGCTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAAC  
TCCCGTGACTTCCTGCGGCACCTCGGCTGCCCTGTCTGGCTCCCCCATGAACCCAGGGCAGCT  
GTGTGAGGTGTGGTTAGACCTGGATCAGGGGAGAAATGGCCAGCTGTACCAGACCTGGGGCA  
GCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGT  
CTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCT  
CTGCTTTGGGGGTGCCCTGCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGT  
GTCACCTGCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTC CATAGGAAGGAGTCTGCC

**FIGURE 225**

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH  
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA  
ILKHLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTA  
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTAFFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF  
FQNMLNLYNFSKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTAFDDQGREYDKEGNLRPWWQNESLA AFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPVAVGLTNHQLFFVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGS PMNPGQLCEVW

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**FIGURE 226A**

GCCCCGGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCCGCTCCCGCGCCCTCCTC  
CCTCCCTCCTCCCCAGCTGTCCCGTTTCGCGTCATGCCGAGCCTCCCGGCCCGCCGGCCCCG  
CTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGGCCCGCGGGCGCCGGCCCCAGAGCC  
CCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCCGTTTCGGGGAGCGGCAGGTAGGT  
GGGCGCCCCGGGGGAGGCGCGGGCGGGGAGTCGGGGCTCGGGGCGAGTCAGCGCCAGCCCCGAG  
GGGGCGCGGGGGCGCAGGTGGCTCGGCGCGGGCGGGCGGCCCGGAGGGTGGGCGGGGGCAGAAG  
GGCGCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGCGGCACACGGCGCGAGCTG  
GGCAGCGGCCTCCAGCCAAGCCCGTCCCCGAGGCTGCACCTTCGGCGGGAAGGTCTATGCC  
TTGGACGAGACGTGGCACCCGGACCTAGGGGAGCCATTCGGGGTGATGCGCTGCGTGCTGTG  
CGCTGCGAGGCGCAGTGGGGTCCCGTACCAGGGGCCCTGGCAGGGTCAGCTGCAAGAACA  
TCAAACCAGAGTGCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGC  
CAGACCTGCCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTTCGAGGCGGTGGCACG  
AGCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCTGGACC  
GCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTTGAGCACCTGCAGCC  
CCCACCAAGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCTCGGTTGTCTCTGCGGCT  
CCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCACCTTCAGGGGAGGTCT  
GGGGCCCTCTCATCCGGCACCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCTGACTCTA  
GAAGGCCCCACCAGCAGGGCGTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGA  
CTCCTTGCATTTTTTTGTGCTCTTCCGAGGCCTTGCAGGACTAACCAGGTTCCCTTGAGGC  
TCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCAGGAA  
CCAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGCTGGG  
GGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTG  
CTGCCAGGAAGAGCTGCGACGTCCTGCAAAGTGTCTTTGTGGGGCTAATGCCCTGATCCCA  
GTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCCTGATCCT  
CCAGGTGCAATTGGTAGGGACAACCAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCCTC  
AGCGGAGGGATCAGCCCACTGTCCTGTGCCACATGGCTGGCCTATCCTCCCCTGCCCCCAGG  
CCGTGGGTATCTGCCCTGGGCTGGGGTGGCCGAGGGGCTCATATGCTGCTGCAGAATGAGCT  
CTTCTGAACGTGGGCACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCAACGTGGCTGCC  
CTGCCCTACTGTGGGGCATAGCGCCCGCCCTGCCCGTGGCCCTAGCAGGAGCCCTGGTGCTA  
CCCCCTGTGAAGAGCCAAGCAGCAGGGCACGCCTGGCTTTCTTGGATAACCACTGTCACCT  
GCACTATGAAGTGCTGCTGGCTGGGCTTGGTGGCTCAGAACAAGGCACTGTCACTGCCACC  
TCCTTGGGCCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAG  
GCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACCTGCTGCGGCACCTGGCAAAGGCATGGC  
TTCCCTGATGATACCAACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCTCTCCTCCC  
AGGTGCACATAGCCAACCAATGTGAGGTTGGCGGACTGCGCCTGGAGGCGGCCGGGGCCGAG  
GGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGCCTGGTCT  
CCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCTGGGCGGGCCCCGAGACCCCAACACATGCT  
TCTTCGAGGGGCAGCAGCGCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGC  
TCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCGCCAG  
CTGCCACACCCGGTGCCAGGCTCCCGACCAGTGCTGCCCTGTTTGCCCTGGCTGCTATTTTG  
ATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCCTTTGGC  
TTAATTAAGTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAA  
GGTGCAGTGTCCCCGGCTGGCCTGTGCCAGCCTGTGCGTGTCAACCCACCCGACTGCTGCA  
AACAGTGTCCAGGTGAGGCCACCCCAAGCTGGGGGACCCATGCAGGCTGATGGGCCCGG  
GGCTGCCGTTTTGTGCTGGGCAGTGGTTCCAGAGAGTCAGAGCTGGCACCCCTCAGTGCCCC  
GTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGTGT  
GAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCAGGGAGGTCCCTGAAGAA  
GCTGAAGGTCACTGTGTCCAGTGCCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTTGTACC  
AGGCAGGGGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGG  
AAGGAGAGTCGATGCTGTTCCCGCTGCACGGCCACCGGCGGCGTAAGTGAGGGAGTCCAGG  
GTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAGGGAAGGGAGCAC  
TCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCTCACAGC  
AACCTGGTGGAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGA  
AATTAAGCAACGAGATGAAGGTCACCCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGC

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**FIGURE 226B**

CTTTCTGGGACCAAGGCAGGGATGCTTTGCCCTGCCCTCTATGCCTCTCTGTGCCTCTCCAC  
TCCCTCTCCCCTCCTCCAACATTCCCTCCCTTCTGTCTCCAGCAGCCCCAGAGACCAGAACT  
GATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCCAAGTGACCA  
AGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCAATTCTCCTGTGG  
GAAGCCCAGTGCCTTTTGCTCCTCTGTCTCCTGCTCTACTCCCACCCCCACTACCTCTGGGAAC  
CACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTCACAGCCACTCCAAGTCCT  
GCCCTGCCACCCTCGGCCTCTGTCTGGAAGCCCCACCCCTTTCTTCCTGTACATAATGTCA  
CTGGCTTGTTGGGATTTTTAATTTATCTTCACTCAGCACCAAGGGCCCCGGACACTCCACTC  
CTGCTGCCCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTTGTATTTATTAAACATTTCT  
TTTTTCAGTCTTTGGGCATGAGGTTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCCTGGTGG  
AGAAGGGGCGAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGA  
CCTGGAGAGGCAGAGGATAGCGTGGCNNTTGGCTGGCATNCCTGGGTTCCGCAGAGGGGCTG  
GGGATGGTTCTTGAGATGGTCTAGAGACTCAAGAATTTAGGGAAGTAGAAGCAGGATTTTGA  
CTCAAGTTTAGTTTCCCACATCGCTGGCCTGTTTGCTGACTTCATGTTTGAAGTTGCTCCAG  
AGAGAGAATCAAAGGTGTCACCAGCCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTTCTTTC  
CCTCCCCTCCCCTCCCCTCCCCTCCCCTCC

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**FIGURE 227**

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCGCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC  
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTGGA  
GGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTCAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAACTGCCCT  
CCTTTCTTTCTTCTTTTCTTCTCCTCCCTCCCTCCCTTTCTTCCCCTTTTCTTCCCTTCCCTTCC  
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTTCACTGTCGATGGGTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCCCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

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**FIGURE 228**

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC  
TTCTATGCCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC  
ACTTCGGCTGCCCTGTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
TTGCTCTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCCACA  
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT  
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTCACCCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTC CATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC